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*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

D Clark

PAGE: 1

RAW SEQUENCE LISTING PATENT APPLICATION US/08/934,254

DATE: 03/25/98 TIME: 16:50:00

INPUT SET: S24406.raw

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

	1	SEQUENCE LISTING
	2	Dogo Alica
	3	(1) General Information: Does Not Comply
	4 5	(i) APPLICANT: Thomas, Terry L. Corrected Diskette Needed
	5 6	(1) APPLICANT: Indinas, Terry L.
	7	
	8	(ii) TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
	9	DELTA 6-DESATURASE
	10	
>	0/11	(iii) NUMBER OF SEQUENCES: 27
	12	
	13	(iv) CORRESPONDENCE ADDRESS:
	14	
	15	(A) ADDRESSEE: Scully, Scott, Murphy & Presser
	16	(B) STREET: 400 Garden City Plaza
	17	(C) CITY: Garden City
	18	(D) STATE: New York (E) COUNTRY: United States
	19 20	(F) ZIP: 11530
	21	(F) HIF. 11550
	22	(v) COMPUTER READABLE FORM:
	23	(V) Controller Renewal Louis
	24	(A) MEDIUM TYPE: Floppy disk
	25	(B) COMPUTER: IBM PC compatible
	26	(C) OPERATING SYSTEM: PC-DOS/MS-DOS
	27	(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
	28	
	29	(vi) CURRENT APPLICATION DATA:
	30	· · · · · · · · · · · · · · · · · · ·
	31	(A) APPLICATION NUMBER:
	32	(B) FILING DATE:
	33	(C) CLASSIFICATION:
	34 35	(viii) ATTORNEY/AGENT INFORMATION:
	35 36	(VIII) ATTORNET/AGENT INFORMATION:
	37	(A) NAME: Presser, Leopold
	38	(B) REGISTRATION NUMBER: 19,827
	39	(C) REFERENCE/DOCKET NUMBER: 8383ZYXWVU
	40	
	41	(ix) TELECOMMUNICATION INFORMATION:
	42	(A) TELEPHONE: (516) 742-4343
	43	(B) TELEFAX: (516) 742-4366
	44	(C) TELEX: 230 901 SANS UR
	45	

RAW SEQUENCE LISTING PATENT APPLICATION US/08/934,254

DATE: 03/25/98 TIME: 16:50:01

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ERRORED SEQUENCES FOLLOW:

	46	(2) INFORMATION FOR SEQ ID NO:1:
	47	
	48	(i) SEQUENCE CHARACTERISTICS:
	49	
>	50	(A) LENGTH: 3588 base pairs
	51	(B) TYPE: nucleic acid
	52	(C) STRANDEDNESS: both
	53	(D) TOPOLOGY: linear
	54	
	55	(ii) MOLECULE TYPE: DNA (genomic)
	56	
	57	(ix) FEATURE:
	58	
	59	(A) NAME/KEY: CDS
	60	(B) LOCATION: 20023081
	61.	Insit em
	62	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: GCTAGCCACC AGTGACGATG CCTTGAATTT GGCCATTCTG ACCCAGGCCC GTATTCTGAA 60 TCCCCGCATT CGCATTGTTA ATCGTTTGTT CAACCATGCC CTGGGTAAAC GTTTAGACAC
	63	
	64	GCTAGCCACC AGTGACGATG CCTTGAATTT GGCCATTCTG ACCCAGGCCC GTATTCTGAA
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	69	CARGEMAGGAA GAGGAAGGMAA GEMMAAAGMAM MEGGGGGGGGAA GAGGGGGGAA MAMAMAMAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG
	70	CACCTTGCCA GACCACGTTA GTTTGAGTGT TTCCGCCCTG GCGGCCCCGA TTTTTTCCTT
	71	180
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	75	240
	75 76	TCAGGAAATT GTCATTCACC AAGACCATCC CTGGCTCAAT TTACCCCTGG CGGATTTATG
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RAW SEQUENCE LISTING PATENT APPLICATION US/08/934,254

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95	TGCAAAAAAG TCAGATAAAA TAAAAGCTTC 1740 CAGGCATCTG CTCTAGGGAG TTTTTCGGC 1800 TAACTCCCCC ATTTTTAGGC AAAATCATAG 1860 ATGACTCACT GTAGAAGGCA GACTAAAAT 1920 TTTAGTCTCC CCCGGCGCTG GAGTTTTTT 1980 TTTATCTATT TAAAATTTATA A ATG CTA 2031 Met Leu 1 CAG AAA CGG GGG TTT CGT CGG GTA 2079 Gln Lys Arg Gly Phe Arg Arg Val 15 TTT GCC GAG CAT GGC CTG ACC CAA 2127 Phe Ala Glu His Gly Leu Thr Gln 30 AAA ACC CTG ATT ATT GTG CTC TGG 2175 Lys Thr Leu Ile Ile Val Leu Trp 45 CTT TTT GCT CCA GTT ATT TTT CCG 2223 Leu Phe Ala Pro Val Ile Phe Pro 60 TTG GCG ATC GCC TTG GCG GCC TTT 2271 Leu Ala Ile Ala Leu Ala Ala Phe 75 AAC CAC AAT GCC TAT TCC TCC AAT 2319 Asn His Asn Ala Tyr Ser Ser Asn	TGCAAAAAAG TCAGATAAAA TAAAAGCTTC ACT 1740 CAGGCATCTG CTCTAGGGAG TTTTTCCGCT GCC 1800 TAACTCCCCC ATTTTTAGGC AAAATCATAT ACT 1860 ATGACTCACT GTAGAAGGCA GACTAAAAATT CTT 1920 TTTAGTCTCC CCCGGCGCTG GAGTTTTTTT GTT 1980 TTTATCTATT TAAATTTATA A ATG CTA ACA 2031 Met Leu Thr 1 CAG AAA CGG GGG TTT CGT CGG GTA CTA 2079 Gln Lys Arg Gly Phe Arg Arg Val Leu 15 TTT GCC GAG CAT GGC CTG ACC CAA AGG 2127 Phe Ala Glu His Gly Leu Thr Gln Arg 30 AAA ACC CTG ATT ATT GTG CTC TGG TTG 2175 Lys Thr Leu Ile Ile Val Leu Trp Leu 45 CTT TTT GCT CCA GTT ATT TTT CCG GTG 2223 Leu Phe Ala Pro Val Ile Phe Pro Val 60 TTG GCG ATC GCC TTG GCG GCC TTT TCC 2271 Leu Ala Ile Ala Leu Ala Ala Phe Ser 75 AAC CAC AAT GCC TAT TCC TCC AAT CCC 2319 Asn His Asn Ala Tyr Ser Ser Asn Pro	TGCAAAAAG TCAGATAAAA TAAAAGCTTC ACTTCGC 1740 CAGGCATCTG CTCTAGGGAG TTTTTCCGCT GCCTTT 1800 TAACTCCCCC ATTTTTAGGC AAAATCATAT ACAGACT 1860 ATGACTCACT GTAGAAGGCA GACTAAAATT CTAGCAA 1920 TTTTAGTCTCC CCCGGCGCTG GAGTTTTTTT GTAGTT 1980 TTTATCTATT TAAATTTATA A ATG CTA ACA GCG 2031 Met Leu Thr Ala 1 CAG AAA CGG GGG TTT CGT CGG GTA CTA AAC 2079 Gln Lys Arg Gly Phe Arg Arg Val Leu Asn 20 TTT GCC GAG CAT GGC CTG ACC CAA AGG GAT 2127 Phe Ala Glu His Gly Leu Thr Gln Arg Asp 30 AAA ACC CTG ATT ATT GTG CTC TGG TTG TTT 2175 Lys Thr Leu Ile Ile Val Leu Trp Leu Phe 45 CTT TTT GCT CCA GTT ATT TTT CCG GTG CGC 2223 Leu Phe Ala Pro Val Ile Phe Pro Val Arg 60 TTG GCG ATC GCC TTG GCG GCC TTT TCC TCC 2271 Leu Ala Ile Ala Leu Ala Ala Phe Ser Phe 75 AAC CAC AAT GCC TAT TCC TCC AAT CCC CAC 2319 Asn His Asn Ala Tyr Ser Ser Asn Pro His 100	TGCAAAAAAG TCAGATAAAA TAAAAGCTTC ACTTCGGTTT 1740 CAGGCATCTG CTCTAGGGAG TTTTTCGCT GCCTTTAGAG 1800 TAACTCCCCC ATTTTAGGC AAAATCATAT ACAGACTATC 1860 ATGACTCACT GTAGAAGGCA GACTAAAATT CTAGCAATGG 1920 TTTAGTCTCC CCCGGCGCTG GAGTTTTTTT GTAGTATATG 1980 TTTATCTATT TAAATTTATA A ATG CTA ACA GCG GAA 2031 Met Leu Thr Ala Glu 1	TGCAAAAAG TCAGATAAAA TAAAAGCTTC ACTTCGGTTT TATA 1740 CAGGCATCTG CTCTAGGGAG TTTTTCCGCT GCCTTTAGAG AGT. 1800 TAACTCCCCC ATTTTTAGGC AAAATCATAT ACAGACTATC CCAL 1860 ATGACTCACT GTAGAAGGCA GACTAAAATT CTAGCAATGG ACTG 1920 TTTAGTCTCC CCCGGCGCTG GAGTTTTTTT GTAGTTAATG GCGC 1980 TTTATCTATT TAAATTTATA A ATG CTA ACA GCG GAA AGA 2031 Met Leu Thr Ala GGu Arg 1	TGCAAAAAAG TCAGATAAAA TAAAAGCTTC ACTTCGGTTT TATATTC 1740 CAGGCATCTG CTCTAGGGAG TTTTTCCGCT GCCTTTAGAG AGTATTT 1800 TAACTCCCCC ATTTTTAGGC AAAATCATAT ACAGACTATC CCAATAT1860 ATGACTCACT GTAGAAGGCA GACTAAAATT CTAGCAATGG ACTCCCAA1920 TTTAGTCTATT TAAAATTTATAA A ATG CTA ACA GCG GAA AGA ATT 2031 Met Leu Thr Ala Glu Arg Ile 1 CAG AAA CGG GGG TTT CGT CGG GTA CTA ACA CAA CGG GTG 2079 Gln Lys Arg Gly Phe Arg Arg Val Leu Asn Gln Arg Val 15 TTT GCC GAG CAT GGC CTG ACC CAA AGG GAT AAT CCC TCC 2127 Phe Ala Glu His Gly Leu Thr Gln Arg Asp Asn Pro Ser 30 AAA ACC CTG ATT ATT GTG CTC TGG TTG TTT TCC GCT TGG 2175 Lys Thr Leu Ile Ile Val Leu Trp Leu Phe Ser Ala Trp 50 CTT TTT GCT CCA GTT ATT TTT CCG GTG CGC CTA CTG GGT 2223 Leu Phe Ala Pro Val Ile Phe Pro Val Arg Leu Leu Gly 60 TTG GCG ATC GCC TTG GCG GCC TTT TCC TTC AAT GTC GGC 2211 ACC CAC AAT GCC TAT TCC TCC AAT CCC CAC ATC ACC CGG ACC 2319 AAA CC CAC AAT GCC TAT TCC TCC AAT CCC CAC ATC AAC CGG ACC 2319 AAA CC CAC AAT GCC TAT TCC TCC AAT CCC CAC ATC AAC CGG ACC 2319 AAC CAC AAT GCC TAT TCC TCC AAT CCC CAC ATC AAC CGG 2319 AAC CAC AAT GCC TAT TCC TCC AAT 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Glu His Gly Leu Thr Gln Arg Asp Asn Pro Ser Met 30 AAA ACC CTG ATT ATT GTG CTC TGG TTG TTT TCC GCT TGG GCC 2175 Lys Thr Leu Ile Ile Val Leu Trp Leu Phe Ser Ala Trp Ala 45 CTT TTT GCT CCA GTT ATT TTT CCG GTG CGC CTA CTG GGT TGT 2223 Leu Phe Ala Pro Val Ile Phe Pro Val Arg Leu Leu Gly Cys 60 TTG GCG ATC GCC TTG GCG GCC TTT TCC TTC AAT GTC GGC CAC 2271 Leu Ala Ile Ala Leu Ala Ala Phe Ser Phe Asn Val Gly His 75 AAC CAC AAT GCC TAT TCC TCC AAT CCC CAC ATC AAC CGG GTT 2319 Asn His Asn Ala Tyr Ser Ser Asn Pro His Ile Asn Arg Val 95	TGCAAAAAAG TCAGATAAAA TAAAAGCTTC ACTTCGGTTT TATATTGTGA CCATC 1740 CAGGCATCTG CTCTAGGGAG TTTTTCCGCT GCCTTTAGAG AGTATTTCT CCAAC 1800 TAACTCCCCC ATTTTTAGGC AAAATCATAT ACAGACTATC CCAATATTGC CAGGC 1860 ATGACTCACT GTAGAAGGCA GACTAAAAAT CTAGCAATGG ACTCCCAGTT GGAAC 1920 TTTAGTCTCC CCCGGCGCTG GAGTTTTTT GTAGTTAATG GCGGTATAAT GTGAAC 1980 TTTATCTATT TAAAATTTATA A ATG CTA ACA GCG GAA AGA ATT AAAA TTT 2031 Met Leu Thr Ala Glu Arg Ile Lys Phe 1	TGCAAAAAAG TCAGATAAAA TAAAAGCTTC ACTTCGGTTT TATATTGTGA CCATGGTTCC 1740 CAGGCATCTG CTCTAGGGAG TTTTTCCGCT GCCTTTAGAG AGTATTTCT CCAAGTCGGC 1800 TAACTCCCCC ATTTTTAGGC AAAATCATAT ACAGACTATC CCAATATTGC CAGAGCTTTG 1860 ATGACTCACT GTAGAAGGCA GACTAAAATT CTAGCAATGG ACTCCCAGTT GGAATAAATT 1920 TTTAGTCTCC CCCGGCGCTG GAGTTTTTT GTAGTTAATG GCGGTATAAT GTGAAAGTT 1980 TTTATCTATT TAAATTTATA A ATG CTA ACA GCG GAA AGA ATT AAA TTT ACC 2031 Met Leu Thr Ala Glu Arg Ile Lys Phe Thr 10 CAG AAA CGG GGG TTT CGT CGG GTA CTA AAC CAA CGG GTG GAT GCC TAC 2079 Cln Lys Arg Gly Phe Arg Arg Val Leu Asn Gln Arg Val Asp Ala Tyr 20 TTT GCC GAG CAT GGC CTG ACC CAA AGG GAT AAT CCC TCC ATG TAT CTG 2127 Phe Ala Glu His Gly Leu Thr Gln Arg Asp Asn Pro Ser Met Tyr Leu 30 AAA ACC CTG ATT ATT GTG CTC TGG TTG TTT TCC GCT TGG GC TTT GTG 2127 Lys Thr Leu Ile Ile Val Leu Trp Leu Phe Ser Ala Trp Ala Phe Val 45 CTT TTT GCC GAG CAT GAT ATT TTT CCG GTG CGC CTA CTG GGT TGT ATG GTT 2223 Leu Phe Ala Pro Val Ile Phe Pro Val Arg Leu Gly Cys Met Val 60 TTG GCG ATC GCC TTG GCG GCC TTT TCC TTC AAT GTC GGC CAC GAT GCC 2271 Leu Ala Ile Ala Leu Ala Ala Phe Ser Phe Asn Val Gly His Asp Ala 75 AAC CAC AAT GCC TAT TCC TCC AAT CCC CAC ATC AAC CGG GTT CTG GGC 2319 AAC CAC AAT GCC TAT TCC TCC AAT CCC CAC ATC AAC CGG GTT CTG GGC 2319 AAC CAC AAT GCC TAT TCC TCC AAT CCC CAC ATC AAC CGG GTT CTG GCC 2319 AAC CAC AAT GCC TAT TCC TCC AAT CCC CAC ATC AAC CGG GTT CTG GCC 2319 AAC CAC AAT GCC TAT TCC TCC AAT CCC CAC ATC AAC CGG GTT CTG GCC 2319 AAC CAC AAT GCC TAT TCC TCC AAT CCC CAC ATC AAC CGG GTT CTG GCC 2319 AAC CAC AAT GCC TAT TCC TCC AAT CCC CAC ATC AAC CGG GTT CTG GCC 2319 AAC CAC AAT GCC TAT TCC TCC AAT CCC CAC ATC AAC CGG GTT CTG GCC 2319 AAC CAC AAT GCC TAT TCC TCC AAT CCC CAC ATC AAC CGG GTT CTG GCC 2319 AAS AS

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200	Met Thr	Tyr	_	Phe	vaı	GTĀ	Leu		Ser	Pne	Leu	ттр		туг	Arg
201			110					115					120		
202	a.aa	m s m	mma	a.a	a.a	3.00	mag	3.00	3 3 777	a mm	amm	aaa	CI A ITT	ava	ama
203	CAC AAC	TAT	TTG	CAC	CAC	ACC	TAC	ACC	AAT	ATT	CIT	GGC	CAT	GAC	GIG
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205	His Asn	-	rea	HIS	HIS	THE	130	THE	ASII	тте	rea	135	птр	ASP	val
206 207		125					130					133			
207	GAA ATC	CAM	aax	CI A ITT	aaa	aa x	CITE A	COM	N TO C	N CITT	CCT	GAA	CAA	CAA	CATE
208	2463	CAI	GGA	GAI	GGC	GCA	GIA	CGI	AIG	AGI	CCI	GAA	CAA	GAA	CAI
210	Glu Ile	uic	al w) an	G1 17	λla	Val	λra	Mo+	Ser	Dro	alu.	G] n	G] 11	Hie
211	140	III	GLY	изр	GLY	145	Val	Arg	Mec	561	150	OLU	01	OLG	1110
212	140					143					130				
213	GTT GGT	יחיתי א	ጥለጥ	ССТ	ጥጥረ	CAG	CAA	արար	πаπ	λητη	TCC	аат	тπъ	тΔт	СФФ
214	2511	AI.	171	CGI	110	CAG	CAA		17.1		100	001			011
215	Val Gly	Tle	Tur	Δra	Phe	Gln	Gln	Phe	Tur	Tle	Trp	ตาง	Leu	Tur	Leu
216	155		-1-	5	160				- , -	165	F			-7-	170
217	100														
218	TTC ATT	ccc	ттт	тат	TGG	ттт	CTC	TAC	GAT	GTC	TAC	СТА	GTG	CTT	AAT
219	2559	-					•••								
220	Phe Ile	Pro	Phe	Tvr	Trp	Phe	Leu	Tvr	Asp	Val	Tvr	Leu	Val	Leu	Asn
221				175	F			-1-	180					185	
222															
223	AAA GGC	AAA	TAT	CAC	GAC	CAT	AAA	ATT	CCT	CCT	TTC	CAG	CCC	CTA	GAA
224	2607														
225	Lys Gly	Lys	Tyr	His	Asp	His	Lys	Ile	Pro	Pro	Phe	Gln	Pro	Leu	Glu
226		•	190		_		_	195					200		
227															
228	TTA GCT	AGT	TTG	CTA	GGG	ATT	AAG	CTA	TTA	TGG	CTC	GGC	TAC	GTT	TTC
229	2655														
230	Leu Ala	Ser	Leu	Leu	Gly	Ile	Lys	Leu	Leu	Trp	Leu	Gly	Tyr	Val	Phe
231		205					210					215			
232															
233	GGC TTA	CCT	CTG	GCT	CTG	GGC	TTT	TCC	ATT	CCŢ	GAA	GTA	TTA	ATT	GGT
234	2703									_					
235	Gly Leu	Pro	Leu	Ala	Leu	_	Phe	Ser	Ile	Pro		Val	Leu	Ile	GTÀ
236	220					225					230				
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238	GCT TCG	GTA	ACC	TAT	ATG	ACC	TAT	GGC	ATC	GTG	GTT	TGC	ACC	ATC	TTT
239	2751		1	_		~ 1		41	-1.	••- •	7	a	m\	- 1 -	Db a
240	Ala Ser	val	Thr	Tyr		Thr	Tyr	GTÀ	тте		vaı	cys	Inr	тте	
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243	ATG CTG	GCC	CAT	GTG	1 1 G	GAA	TCA	ACT	GAA	TTT	Crc	ACC	CCC	GAT	GG.T.
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247	GAA TCC	CCTT	aca	λmm	CIAT	GAG	ava	ጥርረር	QОT	א חייוי	ጥርረ	מאא	Σηνην	ር ር ር	ACC
240	2847	GGI	GCC	WII	GAI	GAC	GAG	100	501	VII	130	CAA	VI.	CG1	ACC
250	Glu Ser	@1 vz	αΙο	٦٦م	Acn	Δen	@lii	Ψrn	Δla	aTT	Cve	Gln	Tle	Ara	Thr
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253	ACG GCC	AAT	TTT	GCC	ACC	AAT	AAT	CCC	TTT	TGG	AAC	TGG	TTT	TGT	GGC
254	2895		_	_	_				_						
255	Thr Ala			Ala	Thr	Asn		Pro	Phe	Trp	Asn	_	Phe	Cys	Gly
256	-	285					290					295			
257															
258	GGT TTA	AAT	CAC	CAA	GTT	ACC	CAC	CAT	CTT	TTC	CCC	AAT	ATT	TGT	CAT
259	2943												_		
260	Gly Leu		His	Gln	Val		His	His	Leu	Phe		Asn	Ile	Cys	His
261	300					305					310				
262															
263	ATT CAC	TAT	CCC	CAA	TTG	GAA	AAT	ATT	ATT	AAG	GAT	GTT	TGC	CAA	GAG
264	2991														
265	Ile His	Tyr	Pro	Gln	Leu	Glu	Asn	Ile	Ile	Lys	Asp	Val	Cys	Gln	Glu
266	315				320					325					330
267															
268	TTT GGT	GTG	GAA	TAT	AAA	GTT	TAT	CCC	ACC	TTC	AAA	GCG	GCG	ATC	GCC
269	3039														
270	Phe Gly	Val	Glu	Tyr	Lys	Val	Tyr	Pro	Thr	Phe	Lys	Ala	Ala	Ile	Ala
271				335					340					345	
272															
273	TCT AAC	TAT	CGC	TGG	CTA	GAG	GCC	ATG	GGC	AAA	GCA	TCG	TGA	CATTO	BCC
274	3088														
275	Ser Asn	Tyr	Arg	Trp	Leu	Glu	Ala	Met	Gly	Lys	Ala	Ser			
276		_	350					355					360		
277															
278	TTGGGAT	TGA	AGCA!	AAATO	G CA	LAAA	rccci	CG	'AAA'	CTA	TGAT	CGA	AGC (CTTTC	CTGTTG
279	3148														
280															
281	CCCGCCG	ACC	AAATO	cccc	A TO	CTG!	ACCAA	AGG	TTG!	TGT	TGGC	ATTC	CT (CAA	CCCAC
282	3208														
283															
284	TTTGAGG	GGG	TTCAT	rtggc	CC GC	CAGT	rtca <i>p</i>	GC1	rgaco	TAG	GAGG	CAA	AGA 1	rtggc	TGATT
285	3268														
286															
287															
	TTGCTCA	ААТ	CCGCT	rggg <i>i</i>	AT AT	TGA!	AAGGC	TTC	CACC	ACCT	TTGG	TTTC	CTA (CCTC	CTCAA
288	TTGCTCA 3328	ААТ	CCGCT	rggg <i>i</i>	AT AT	TTGA!	AAGGC	TTC	CACC	ACCT	TTGG	STTTC	CTA (CCTC	CTCAA
288 289		ААТ	CCGCT	rggg <i>i</i>	AT AT	TTGA <i>l</i>	AAGGC	TTC	CACCA	ACCT	TTGG	TTTC	CTA (CCTC	ECTCAA
289	3328														
289 290	3328 TGGGAAG														
289 290 291	3328 TGGGAAG	GAC	AAACG	CGTC <i>i</i>	AG AA	\TTG7	T TTA T	TC	rggto	BACA	CCAT	CACC	CGA (CCAT	CCATG
289 290 291 292 293	3328 TGGGAAG 3388 TGGTCTA	GAC	AAACG	CGTC <i>i</i>	AG AA	\TTG7	T TTA T	TC	rggto	BACA	CCAT	CACC	CGA (CCAT	CCATG
289 290 291 292 293 294	3328 TGGGAAG 3388	GAC	AAACG	CGTC <i>i</i>	AG AA	\TTG7	T TTA T	TC	rggto	BACA	CCAT	CACC	CGA (CCAT	CCATG
289 290 291 292 293 294 295	3328 TGGGAAG 3388 TGGTCTA 3448	GAC ACC	AAACC	CGTC <i>i</i>	AG AA	ATTGT	TTTAT	TC1	rggt(BACA BCCA	CCAT	CACC	CGA (CCAC	CCATG BAGGCT
289 290 291 292 293 294 295 296	3328 TGGGAAG 3388 TGGTCTA 3448 AGGCCAG	GAC ACC	AAACC	CGTC <i>i</i>	AG AA	ATTGT	TTTAT	TC1	rggt(BACA BCCA	CCAT	CACC	CGA (CCAC	CCATG BAGGCT
289 290 291 292 293 294 295 296 297	3328 TGGGAAG 3388 TGGTCTA 3448	GAC ACC	AAACC	CGTC <i>i</i>	AG AA	ATTGT	TTTAT	TC1	rggt(BACA BCCA	CCAT	CACC	CGA (CCAC	CCATG BAGGCT
289 290 291 292 293 294 295 296 297 298	3328 TGGGAAG 3388 TGGTCTA 3448 AGGCCAG 3508	GAC ACC AAA	AAACC CAGCC	CGTC!	AG AA	attgt aagge	PTTAT	TCT	rggto Caago	BACA BCCA BGCT	CCAT TGC	CACC	CCTA (CCAT	CCATG BAGGCT TTTTTG
289 290 291 292 293 294 295 296 297 298 299	3328 TGGGAAG 3388 TGGTCTA 3448 AGGCCAG 3508 AGCATTT	GAC ACC AAA	AAACC CAGCC	CGTC!	AG AA	attgt aagge	PTTAT	TCT	rggto Caago	BACA BCCA BGCT	CCAT TGC	CACC	CCTA (CCAT	CCATG BAGGCT TTTTTG
289 290 291 292 293 294 295 296 297 298 299 300	3328 TGGGAAG 3388 TGGTCTA 3448 AGGCCAG 3508	GAC ACC AAA	AAACC CAGCC	CGTC!	AG AA	attgt aagge	PTTAT	TCT	rggto Caago	BACA BCCA BGCT	CCAT TGC	CACC	CCTA (CCAT	CCATG BAGGCT TTTTTG
289 290 291 292 293 294 295 296 297 298 299 300 301	TGGGAAG 3388 TGGTCTA 3448 AGGCCAG 3508 AGCATTT 3568	GAC ACC AAA TTG	AAACC CAGCC AATTA	CGTCA CCTGC	AG AAG CA	attgt aagge	PTTAT	TCT	rggto Caago	BACA BCCA BGCT	CCAT TGCA	CACC	CCTA (CCAT	CCATG BAGGCT TTTTTG
289 290 291 292 293 294 295 296 297 298 299 300 301 302	TGGGAAG 3388 TGGTCTA 3448 AGGCCAG 3508 AGCATTT 3568 AATTTTA	GAC ACC AAA TTG	AAACC CAGCC AATTA	CGTCA CCTGC	AG AAG CA	attgt aagge	PTTAT	TCT	rggto Caago	BACA BCCA BGCT	CCAT TGCA	CACC	CCTA (CCAT	CCATG BAGGCT TTTTTG
289 290 291 292 293 294 295 296 297 298 299 300 301	TGGGAAG 3388 TGGTCTA 3448 AGGCCAG 3508 AGCATTT 3568	GAC ACC AAA TTG	AAACC CAGCC AATTA	CGTCA CCTGC	AG AAG CA	attgt aagge	PTTAT	TCT	rggto Caago	BACA BCCA BGCT	CCAT TGCA	CACC	CCTA (CCAT	CCATG BAGGCT TTTTTG

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	305		INPU1 SE1: S24400.raw
	388	(2) INFORMATION FOR SEQ ID NO:3:	
	389		
	390	(i) SEQUENCE CHARACTERISTICS:	
	391		
>	392	(A) LENGTH: 1884 base pairs	
	393	(B) TYPE: nucleic acid	
	394	(C) STRANDEDNESS: both	
	395	(D) TOPOLOGY: linear	· WC
	396		same
	397	(ii) MOLECULE TYPE: DNA (genomic)	10
	398		,
	399	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
	400		
	401	AGCTTCACTT CGGTTTTATA TTGTGACCAT GGTTCCCAGG CATCTGCTC	CT AGGGAGTTTT
	402	60	
	403		
	404	TCCGCTGCCT TTAGAGAGTA TTTTCTCCAA GTCGGCTAAC TCCCCCATT	TT TTAGGCAAAA
	405	120	
	406		
	407	TCATATACAG ACTATCCCAA TATTGCCAGA GCTTTGATGA CTCACTGTA	AG AAGGCAGACT
	408	180	
	409		
	410	AAAATTCTAG CAATGGACTC CCAGTTGGAA TAAATTTTTA GTCTCCCCC	CG GCGCTGGAGT
	411	240	
	412		
	413	TTTTTTGTAG TTAATGGCGG TATAATGTGA AAGTTTTTTA TCTATTTAA	AA TTTATAAATG
	414	300	
	415		
	416	CTAACAGCGG AAAGAATTAA ATTTACCCAG AAACGGGGGT TTCGTCGGC	GT ACTAAACCAA
	417	360	
	418		
	419	CGGGTGGATG CCTACTTTGC CGAGCATGGC CTGACCCAAA GGGATAATC	C CTCCATGTAT
	420	420	
	421		THE COMMUNICATION
	422 423	CTGAAAACCC TGATTATTGT GCTCTGGTTG TTTTCCGCTT GGGCCTTTC 480	or Gerringer
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	428	TTTTCCTTCA ATGTCGGCCA CGATGCCAAC CACAATGCCT ATTCCTCCA	א שרכככאראשר
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	431	AACCGGGTTC TGGGCATGAC CTACGATTTT GTCGGGTTAT CTAGTTTTC	ጣ ጥጥርርርርርጥልጥ
	432	660	
	433	***	
	434	CGCCACAACT ATTTGCACCA CACCTACACC AATATTCTTG GCCATGACC	T GGAAATCCAT
	435	720	
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	437	GGAGATGGCG CAGTACGTAT GAGTCCTGAA CAAGAACATG TTGGTATTT	'A TCGTTTCCAG
	438	780	
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437						
440 441	CAATTTTATA 840	TTTGGGGTTT	ATATCTTTTC	ATTCCCTTTT	ATTGGTTTCT	CTACGATGTC
442 443 444	TACCTAGTGC 900	TTAATAAAGG	CAAATATCAC	GACCATAAAA	TTCCTCCTTT	CCAGCCCCTA
445 446 447	GAATTAGCTA 960	GTTTGCTAGG	GATTAAGCTA	TTATGGCTCG	GCTACGTTTT	CGGCTTACCT
448 449 450	CTGGCTCTGG	GCTTTTCCAT	TCCTGAAGTA	TTAATTGGTG	CTTCGGTAAC	CTATATGACC
451 452	TATGGCATCG	TGGTTTGCAC	CATCTTTATG	CTGGCCCATG	TGTTGGAATC	AACTGAATTT
453 454 455	1080 CTCACCCCG	ATGGTGAATC	CGGTGCCATT	GATGACGAGT	GGGCTATTTG	CCAAATTCGT
456 457 458	1140 ACCACGGCCA	ATTTTGCCAC	CAATAATCCC	TTTTGGAACT	GGTTTTGTGG	CGGTTTAAAT
459 460	1200	GGGA GGAMGM	mmmaaaa a a a m		mma a ama maa	CC A A TITUCCA A
461 462 463	1260	CCCACCATCT	TTTCCCCAAT	ATTTGTCATA	TTCACTATCC	CCAATTGGAA
464 465 466	AATATTATTA 1320	AGGATGTTTG	CCAAGAGTTT	GGTGTGGAAT	ATAAAGTTTA	TCCCACCTTC
467 468	AAAGCGGCGA 1380	TCGCCTCTAA	CTATCGCTGG	CTAGAGGCCA	TGGGCAAAGC	ATCGTGACAT
469 470 471	TGCCTTGGGA	TTGAAGCAAA	ATGGCAAAAT	CCCTCGTAAA	TCTATGATCG	AAGCCTTTCT
472 473 474	GTTGCCCGCC	GACCAAATCC	CCGATGCTGA	CCAAAGGTTG	ATGTTGGCAT	TGCTCCAAAC
475 476 477	CCACTTTGAG	GGGGTTCATT	GGCCGCAGTT	TCAAGCTGAC	CTAGGAGGCA	AAGATTGGGT
478 479 480	GATTTTGCTC 1620	AAATCCGCTG	GGATATTGAA	AGGCTTCACC	ACCTTTGGTT	TCTACCCTGC
481 482		GGACAAACCG	TCAGAATTGT	TTATTCTGGT	GACACCATCA	CCGACCCATC
483 484 485	1680	AACCCAGCCC	TGGCCAAGGC	TTGGACCAAG	GCCATGCAAA	TTCTCCACGA
486 487	1740					
488 489 490	1800	GAAAAATTAT	ATTGGCTCCT	GATTTCTTCC	GGCTATCGCA	CCTACCGATT
491	TTTGAGCATT	TTTGCCAAGG	AATTCTATCC	CCACTATCTC	CATCCCACTC	CCCCGCCTGT

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	494		ATCCATCAGC	TAGC				
	495	1884						
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	498	(2) THEODY	AMTON HOD CI	TO TO MO. 4.	···			
	498	(2) INFORM	ATION FOR SI	EQ ID NO:4:				
	500	/il ci	EQUENCE CHAI		٥.			
	501	(I) Si	EQUENCE CHAI	RACIERISTIC	.			
>	502		(A) LENGTH:	160E hage	naire			
/	502		(B) TYPE: nu		harra			
	504		(C) STRANDEI					
	505		(D) TOPOLOGY					
	506		(D) TOPOLOG.	. Tinear				
	507	(ii) M	OLECULE TYPE	E: DNA (den	omic)			<i>رو</i> په
	508	(11)		2. 2 (90	J20 ,			Same
	509	(xi) S	EQUENCE DESC	CRIPTION: SI	EO ID NO:4:			/ /
	510	(,	-20-110- 5-5					•
	511	AATATCTGCC	TACCCTCCCA	AAGAGAGTAG	TCATTTTTCA	TCAATGGCTG	CTCAAATCAA	
	512	60						
	513							
	514	GAAATACATT	ACCTCAGATG	AACTCAAGAA	CCACGATAAA	CCCGGAGATC	TATGGATCTC	
	515	120						
	516							
	517	GATTCAAGGG	AAAGCCTATG	ATGTTTCGGA	TTGGGTGAAA	GACCATCCAG	GTGGCAGCTT	
	518	180						
	519							
	520	TCCCTTGAAG	AGTCTTGCTG	GTCAAGAGGT	AACTGATGCA	TTTGTTGCAT	TCCATCCTGC	
	521	240						
	522							
	523	CTCTACATGG	AAGAATCTTG	ATAAGTTTTT	CACTGGGTAT	TATCTTAAAG	ATTACTCTGT	
	524	300						
	525							
	526	TTCTGAGGTT	TCTAAAGATT	ATAGGAAGCT	TGTGTTTGAG	TTTTCTAAAA	TGGGTTTGTA	
	527	360	· ·					
	528							
	529		GGTCATATTA	TGTTTGCAAC	TTTGTGCTTT	ATAGCAATGC	TGTTTGCTAT	
	530	420						
	531							
	532		GGGGTTTTGT	TTTGTGAGGG	TGTTTTGGTA	CATTTGTTTT	CTGGGTGTTT	
	533	480						
	534	a. maaaaammm	ammmaamma		a.mmaa.a.m	a.maamaaaa		
	535		CTTTGGATTC	AGAGTGGTTG	GATTGGACAT	GATGCTGGGC	ATTATATGGT	
	536	540						
	537) CINCIDICIDIC E III	maxxaaamm*	3 m 3 3 cmmm 3 m		COMOCARAMO	CITICITITITIC & C.C.	
	538		TCAAGGCTTA	ATAAGTTTAT	GGGTATTTTTT	GCTGCAAATT	GTCTTTCAGG	
	539	600						
	540 541	3 3 M 3 3 CM 3 M M	GGTTGGTGGA	3 3 TCC	па апостасти	СУСУШШСССШ	ста апассоп	
	541		GGIIGGTGGA	AATGGAACCA	TAATGCACAT	CACATTGCCT	GIAAIAGCCT	
	542	660						
	543							

RAW SEQUENCE LISTING PATENT APPLICATION US/08/934,254

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					1	INPU1 SE1: S244
544 545	TGAATATGAC 720	CCTGATTTAC	AATATATACC	ATTCCTTGTT	GTGTCTTCCA	AGTTTTTTGG
546						
547		TCTCATTTCT	ATGAGAAAAG	GTTGACTTTT	GACTCTTTAT	CAAGATTCTT
548	780					
549	шаша а ашшаш	GA A GA MINGGA	C A MMMMM A GGG	mammamamam	GGTGGTT GGG	ma s s m s mams
550 551	TGTAAGTTAT 840	CAACATTGGA	CATTTTACCC	TATTATGTGT	GCTGCTAGGC	TCAATATGTA
551 552	040					
553	ТСТАСААТСТ	CTCATAATGT	ТСТТСАССАА	GAGAAATGTG	ТССТАТССАС	CTCAGGAACT
554	900					
555						
556	CTTGGGATGC	CTAGTGTTCT	CGATTTGGTA	CCCGTTGCTT	GTTTCTTGTT	TGCCTAATTG
557	960					
558						
559	GGGTGAAAGA	ATTATGTTTG	TTATTGCAAG	TTTATCAGTG	ACTGGAATGC	AACAAGTTCA
560	1020					
561						
562		AACCACTTCT	CTTCAAGTGT	TTATGTTGGA	AAGCCTAAAG	GGAATAATTG
563	1080					
564	OMMMOR OR R. R.	CAAACGGATG	CON CACTORIO	a s mmmammam	COMCOMMOGR	maa a mmaamm
565 566	1140	CAAACGGATG	GGACACTTGA	CATTTCTTGT	CCTCCTTGGA	TGGATTGGTT
567	1140					
568	тсатестеса	TTGCAATTCC	AAATTGAGCA	ТСАТТТСТТТ	CCCAAGATGC	СТАСАТССАА
569	1200	1100///1100	AAATTOACCA	1011110111	CCOMMONICO	CINONICONN
570						
571	CCTTAGGAAA	ATCTCGCCCT	ACGTGATCGA	GTTATGCAAG	AAACATAATT	TGCCTTACAA
572	1260			•		
573						
574	TTATGCATCT	TTCTCCAAGG	CCAATGAAAT	GACACTCAGA	ACATTGAGGA	ACACAGCATT
575	1320					
576						
577		GATATAACCA	AGCCGCTCCC	GAAGAATTTG	GTATGGGAAG	CTCTTCACAC
578	1380					
579 580	ma a maamma a	AATTACCCTT	A CITITICA TICITA	3 M 3 A M M M M A A A	3 mm 3 mcm 3 mc	maama mammm
581	1440	AATTACCCTT	AGTICATGTA	ATAATTIGAG	ATTATGTATC	TCCTATGTTT
582	1440					
583	СТСТСТТСТС	TTGGTTCTAC	ттсттссаст	САТТССААСТ	тαтстттт	GGጥጥጥ ል ጥጥልG
584	1500			0		
585	2000					
586	ATGTTTTTTA	ATATATTTTA	GAGGTTTTGC	TTTCATCTCC	ATTATTGATG	AATAAGGAGT
587	1560					
588						
589	TGCATATTGT	CAATTGTTGT	GCTCAATATC	TGATATTTTG	GAATGTACTT	TGTACCACTG
590	1620					
591						
592		TGAAGCTCAT	GTGTACTTCT	ATAGACTTTG	TTTAAATGGT	TATGTCATGT
593	1680					
594 505	та пот					
595 596	TATTT 1685					
370	1002					

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(2) INFORMATION FOR SEQ ID NO:25: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 5 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: Peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: His Val Pro His His 1053 (2) INFORMATION FOR SEQ ID NO:26: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1702 base pairs 1057 0 (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 48..1406 (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 48..1406 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26: CCCCAAAAAT TTTCATTGTT CTCCATCTGG ACCACAGCAT CCACACA ATG GAG GGC Met Glu Gly GAA GCT AAG AAG TAT ATC ACG GCG GAG GAC CTC CGC CGC CAC AAC AAG Glu Ala Lys Lys Tyr Ile Thr Ala Glu Asp Leu Arg Arg His Asn Lys TCC GGC GAT CTC TGG ATC TCC ATC CAG GGC AAG GTC TAC GAC TGC TCT Ser Gly Asp Leu Trp Ile Ser Ile Gln Gly Lys Val Tyr Asp Cys Ser

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													II	VPUI	SEI: S
1087 1088	CGG TGG	aca	aca	CAC	CAC	aaa	aaa	aaa	GAG	QTIC.	aaa	CTC	CTC	λαm	CTC
1089	200	GCG	GCG	GAG	CAC		GGC	GGC	GAG	GIC	CCG	CIC	CIC	AGI	CIG
1099	Arg Trp	λla	λla	Glu.	Hie	Dro	G] v	G1 v	Glu.	Val	Dro	T.011	T.011	Sor	Len
1090	Arg IIp	ALG	ALG	40	птэ	PIO	СТУ	GLY	45	Val	FIU	пец	Leu	50	Leu
1091				40					43					30	
	000 000	a.a	ana	ama	3.00	ana	aaa	mma	a mm	000	шха	ana	aaa	000	Maa
1093	GCC GGC	CAG	GAC	GIC	ACC	GAC	GCC	TIC	ATT	GCG	TAC	CAC	CCG	GGC	ACG
1094	248	a 1 =	1	**- 7	m1	1		Dh.	- 1 -			***	D	al	mb
1095	Ala Gly	GIN		vaT	Thr	ASP	Ата		тте	АТА	Tyr	HIS		GTÄ	THE
1096			55					60					65		
1097	aga maa	000	a a m	ama	алт	000	ama	mma	3.00	000	шаа	ma a	шъс	ama	330
1098 1099	GCG TGG 296	CGG	CAT	CTG	GAT	CCG	CTC	TTC	ACC	GGC	TAC	TAC	TAC	CTC	AAG
			774	T	3	D	T	Db.	mb	a 1	M	M	m	T	T
1100	Ala Trp		urs	Leu	ASP	PIO	75	Pne	THE	СТУ	Tyr		Tyr	Leu	гаг
1101 1102		70					75					80			
	ara mma	a. .	аша	шаа	a.a	3 mg	maa		a.a	mag	000	3.00	amm	mma	330
1103	GAC TTC	GAA	GIG	TCG	GAG	ATC	TCC	AAG	GAC	TAC	CGG	AGG	CIT	TIG	AAC
1104	344 Asp Phe	a1	W-1	C	a1	T1.	C0 =	T	1 ~~	m	X ~~ ~	X	T 011	T 011	3 ~ ~
1105	_	GIU	vaı	Ser	GIU	90	Ser	гуѕ	ASP	Tyr	95	Arg	Leu	Leu	ASII
1106 1107	85					90					93				
1107	GAG ATG	maa	aaa	maa	aaa	х ПС	ттс	CAC	880	220	aaa	CAC	CAC	N TO C	איזיימ
1108	392	100	CGG	100	GGG	AIC	110	GAG	AAG	MAG	GGC	CAC	CAC	AIC	AIG
1110	Glu Met	202	A ra	Cor	C1 17	т1.	Dho	<i>α</i> 1	Lvc	Tue	al v	uie	wie	Tla	Mat
1111	100	Ser	Arg	Ser	105	TTE	FIIE	GIU	пуs	110	GLY	1112	HITS	TTG	115
1112	100				103					110					113
1112	TGG ACG	mma	OTT C	aaa	C TP TP	aaa	OTIO	אשמ	A TO C	aaa	CCA	A TO	ama	ma.c	aaa
1113	440	110	GIC	GGC	GII	·GCG	GIC	AIG	AIG	GCG	GCA	AIC	GIC	IAC	GGC
1115	Trp Thr	Dho	Val	@1 ₁₇	t/a l	λ Ι a	Val	Mot	Mot	λla	λla	т1 о	Wal.	Птт	C 1 11
1116	IIP IIII	FIIC	Val	120	Val	AIG	Val	Mec	125	ALG	AIG	116	Val	130	GLY
1117				120					123					130	
1117	GTG CTG	aca	ጥሮር	GAG	שרכ	CTC	CCA	ርጥጥ	מאת	λπα	כיויכי	ጥርር	GGC	CCA	СТС
1119	488	GCG	100	GAG	100	GIC	GGA	G11	CAC	AIG	CIC	100	GGC	GCA	CIG
1120	Val Leu	λla	Ser	Glu	Ser	Val	Glv	Val	His	Met	T.em	Cvs	Glv	Δla	Len
1121	var nea	n_u	135	O_Lu	501	, u _	0 ±3	140				0,5	145	n_u	200
1122			100					110					143		
1123	CTG GGC	ጥጥር	СТС	TGG	АТС	CAA	GCC	gcg	ጥ Δጥ	GTG	GGC	САТ	GAC	TCC	GGC
1124	536		•••			V									
1125	Leu Gly	Leu	Leu	Trp	Ile	Gln	Ala	Ala	Tvr	Val	Glv	His	Asp	Ser	Glv
1126		150		P			155		-1-		1	160			1
1127															
1128	CAT TAC	CAG	стс	ΔТС	CCA	ACC	CGT	GGA	TAC	AAC	AGA	АТС	ACG	CAA	СТС
1129	584	00			••••		•••	••••						4	
1130	His Tyr	Gln	Val	Met	Pro	Thr	Ara	Glv	Tvr	Asn	Ara	Ile	Thr	Gln	Leu
1131	165					170	• 5	1	-1-		175				
1132	200					•					- · •				
1132	ATA GCA	GGC	AAC	АТС	СТА	ACC	GGA	АТС	AGC	ATC	gcg	TGG	TGG	AAG	TGG
1134	632														
1135	Ile Ala	G] v	Asn	Πle	Leu	Thr	G] v	Ile	Ser	Ile	Ala	Tro	Trp	Lvs	Trp
1136	180	1			185		1			190			E	-1-	195
1137															-
1138	ACC CAC	AAC	GCC	CAC	CAC	CTC	GCC	TGC	AAC	AGC	CTC	GAC	TAC	GAC	CCC
1139	680														
	500														

same

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													I	NPUT	SET: S
1140 1141	Thr His	Asn	Ala	His 200	His	Leu	Ala	Cys	Asn 205	Ser	Leu	Asp	Tyr	Asp 210	Pro
1142 1143 1144	GAC CTC 728	CAG	CAC	ATC	CCC	GTA	TTC	GCC	GTC	TCC	ACC	CGA	CTC	TTC	AAC
1145 1146	Asp Leu	Gln	His 215	Ile	Pro	Val	Phe	Ala 220	Val	Ser	Thr	Arg	Leu 225	Phe	Asn
1147 1148 1149	TCC ATC	ACC	TCG	GTC	TTC	TAT	GGC	CGA	GTC	CTG	AAA	TTC	GAC	GAA	GTG
1150 1151 1152	Ser Ile	Thr 230	Ser	Val	Phe	Tyr	Gly 235	Arg	Val	Leu	Lys	Phe 240	Asp	Glu	Val
1153 1154	GCA CGG 824	TTC	CTA	GTC	AGC	TAC	CAG	CAC	TGG	ACC	TAC	TAC	CCG	GTC	ATG
1155 1156 1157	Ala Arg 245	Phe	Leu	Val	Ser	Tyr 250	Gln	His	Trp	Thr	Tyr 255	Tyr	Pro	Val	Met
1158 1159	ATC TTC 872														
1160 1161 1162	Ile Phe 260	Gly	Arg	Val	Asn 265	Leu	Phe	Ile	Gln	Thr 270	Phe	Leu	Leu	Leu	Leu 275
1163 1164	ACC AGG 920	CGC	GAC	GTC	CCT	GAC	CGC	GCT	CTA	AAC	TTA	ATG	GGT	ATC	GCG
1165 1166 1167	Thr Arg	Arg	Asp	Val 280	Pro	Asp	Arg	Ala	Leu 285	Asn	Leu	Met	Gly	Ile 290	Ala
1168 1169	GTT TTC 968	TGG	ACG	TGG	TTC	CCG	CTC	TTC	GTA	TCT	TGT	CTC	CCG	AAC	TGG
1170 1171 1172	Val Phe	Trp	Thr 295	Trp	Phe	Pro	Leu	Phe 300	Val	Ser	Cys	Leu	Pro 305	Asn	Trp
1173 1174	CCT GAA 1016														
1175 1176 1177	Pro Glu	Arg 310	Phe	Gly	Phe	Val	Leu 315	Ile	Ser	Phe	Ala	Val 320	Thr	Ala	Ile
1178 1179	CAG CAC 1064														
1180 1181 1182	Gln His 325	Val	Gln	Phe	Thr	Leu 330	Asn	His	Phe	Ser	Gly 335	Asp	Thr	Tyr	Val
1183 1184	GGC CCC 1112														
1185 1186 1187	Gly Pro 340	Pro	Lys	Gly	Asp 345	Asn	Trp	Phe	Glu	Lys 350	Gln	Thr	Lys	Gly	Thr 355
1188 1189	ATC GAT 1160	ATC	ACG	TGC	CCA	CCG	TGG	ATG	GAC	TGG	TTC	TTT	GGT	GGG	CTG
1190 1191 1192	Ile Asp	Ile	Thr	Cys 360	Pro	Pro	Trp	Met	Asp 365	Trp	Phe	Phe	Gly	Gly 370	Leu

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														VPUI	SEI: .	5244U0.raw
1193	CAG TTC	CAG	TTG	GAG	CAC	CAC	TTG	TTC	CCT	AGG	CTG	CCG	CGT	GGG	CAG	
1194	1208													_	_	
1195	Gln Phe	Gln		Glu	His	His	Leu		Pro	Arg	Leu	Pro	_	Gly	Gln	
1196			375					380					385			
1197																
1198	CTT AGG	AAG	ATT	GCG	CCC	TTG	GCT	CGG	GAC	TTG	TGT	AAG	AAG	CAC	GGG	
1199	1256		_	_			_							_	_	
1200	Leu Arg	_	Ile	Ala	Pro	Leu		Arg	Asp	Leu	Cys	_	Lys	His	Gly	
1201		390					395					400				10
1202																sin
1203	ATG CCG	TAT	AGG	AGC	TTC	GGG	TTT	TGG	GAC	GAC	GCT	AAT	GTC	AGG	ACA) -
1204	1304				_								_		_	
1205	Met Pro	_	Arg	Ser	Phe	_	Phe	Trp	Asp	Asp		Asn	Val	Arg	Thr	
1206	405					410					415					
1207																
1208	ATT CGG	ACG	CTG	AGG	GAT	GCG	GCG	GTT	CAG	GCG	CGT	GAC	CTT	AAT	TCG	
1209	1352															
1210	Ile Arg	Thr	Leu	Arg	_	Ala	Ala	Val	Gln		Arg	Asp	Leu	Asn		
1211	420				425					430					435	
1212																
1213	GCC CCG	TGC	CCT	AAG	AAA	CTT	GGG	TAT	GGG	GAA	GCT	TAT	AAC	ACC	CAT	
1214	1400															
1215	Ala Pro	Cys	Pro		Lys	Leu	Gly	Tyr	_	Glu	Ala	Tyr	Asn		His	
1216				440					445					450		
1217																
1218	GGT TGA	TTG'	rggt	rtt (TGT'	CTGC	G T	rggac	GATO	TTC	TTAT	TAT	TGAT	rtta:	TGT	
1219	1456															
1220	Gly *															
1221																
1222																
1223	CCACAAT	ATT (GAACT	rgaai	ra ac	CAT	GGAAC	GC.	ACTAC	CGTT	CAG	ATTC	CT 7	rtgci	TAAC	T
1224	1516															
1225														·		
1226	TTGCTAG	CTG (GTTGC	CGTTC	CC CI	TGT	rgggc	GCA	AAAGI	rgca	GTAT	[ATT]	TTT	rctt?	ATCCC	A
1227	1576															
1228																
1229	TGTACTT	TTT (GATT!	ATTGT	rt Ci	TAT	rcgt <i>i</i>	TC.	ATAA!	AATA	TTTI.	LATTA	TG A	ATTA	ATTTT	T
1230	1636															
1231																
1232	GTTGTAG	TTG (GTG?	CTAT	CA GC	CAAG	PATT!	' AA'	CACTO	BAGA	TAT	TTTT	TT.	rggt <i>i</i>	AAAA	A
1233	1696															
1234																
1235	AAAAA															
1236	1702															
1237																
1238																

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1240 1241

1242

1243

1239 (2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 452 amino acids

(B) TYPE: amino acid

1244 (D) TOPOLOGY: linear

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1245 1246		(:	Li) N	MOLE	CULE	TYPI	E: pi	rote:	in								
1247 1248 1249		(2	ki) S	SEQUI	ENCE	DESC	CRIP	CION	: SE(D ID	27:						
1250 1251 1252	Met 1	Glu	Gly	Glu	Ala 5	Lys	Lys	Tyr	Ile	Thr 10	Ala	Glu	Asp	Leu	Arg 15	Arg	
1252 1253 1254 1255	His	Asn	Lys	Ser 20	Gly	Asp	Leu	Trp	Ile 25	Ser	Ile	Gln	Gly	Lys 30		Tyr	
1256 1257 1258	Asp	Cys	Ser 35	Arg	Trp	Ala	Ala	Glu 40	His	Pro	Gly	Gly	Glu 45	Val	Pro	Leu	
1259 1260 1261	Leu	Ser 50	Leu	Ala	Gly	Gln	Asp 55	Val	Thr	Asp	Ala	Phe 60	Ile	Ala	Tyr	His	
1262 1263 1264	Pro 65	Gly	Thr	Ala	Trp	Arg 70	His	Leu	Asp	Pro	Leu 75	Phe	Thr	Gly	Tyr	Tyr 80	
1265 1266 1267	Tyr	Leu	Lys	Asp	Phe 85	Glu	Val	Ser	Glu	Ile 90	Ser	Lys	Asp	Tyr	Arg 95	Arg	
1268 1269 1270	Leu	Leu	Asn	Glu 100	Met	Ser	Arg	Ser	Gly 105	Ile	Phe	Glu	Lys	Lys 110	Gly	His	
1271 1272 1273	His	Ile	Met 115	Trp	Thr	Phe	Val	Gly 120	Val	Ala	Val	Met	Met 125	Ala	Ala	Ile	
1274 1275 1276	Val	Tyr 130	Gly	Val	Leu	Ala	Ser 135	Glu	Ser	Val	Gly	Val 140	His	Met	Leu	Cys	
1277 1278 1279	Gly 145	Ala	Leu	Leu	Gly	Leu 150	Leu	Trp	Ile	Gln	Ala 155	Ala	Tyr	Val	Gly	His 160	
1280 1281 1282	Asp	Ser	Gly	His	Туг 165	Gln	Val	Met	Pro	Thr 170	Arg	Gly	Tyr	Asn	Arg 175	Ile	
1283 1284 1285	Thr	Gln	Leu	Ile 180	Ala	Gly	Asn	Ile	Leu 185	Thr	Gly	Ile	Ser	Ile 190	Ala	Trp	
1286 1287 1288	Trp	Lys	Trp 195	Thr	His	Asn	Ala	His 200	His	Leu	Ala	Cys	Asn 205	Ser	Leu	Asp	
1289 1290 1291	Tyr	Asp 210	Pro	Asp	Leu	Gln	His 215	Ile	Pro	Val	Phe	Ala 220	Val	Ser	Thr	Arg	
1292 1293 1294	Leu 225	Phe	Asn	Ser	Ile	Thr 230	Ser	Val	Phe	Tyr	Gly 235	Arg	Val	Leu	Lys	Phe 240	
1295 1296 1297	Asp	Glu	Val	Ala	Arg 245	Phe	Leu	Val	Ser	Tyr 250	Gln	His	Trp	Thr	Tyr 255	Tyr	

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1298 1299 1300	Pro	Val	Met	Ile 260	Phe	Gly	Arg	Val	Asn 265	Leu	Phe	Ile	Gln	Thr 270		Leu
1301 1302 1303	Leu	Leu	Leu 275	Thr	Arg	Arg	Asp	Val 280	Pro	Asp	Arg	Ala	Leu 285	Asn	Leu	Met
1304 1305 1306	Gly	Ile 290	Ala	Val	Phe	Trp	Thr 295	Trp	Phe	Pro	Leu	Phe 300	Val	Ser	Cys	Leu
1307 1308 1309	Pro 305	Asn	Trp	Pro	Glu	Arg 310	Phe	Gly	Phe	Val	Leu 315	Ile	Ser	Phe	Ala	Val 320
1310 1311 1312	Thr	Ala	Ile	Gln	His 325	Val	Gln	Phe	Thr	Leu 330	Asn	His	Phe	Ser	Gly 335	Asp
1313 1314 1315	Thr	Tyr	Val	Gly 340	Pro	Pro	Lys	Gly	Asp 345	Asn	Trp	Phe	Glu	Lys 350	Gln	Thr
1316 1317 1318	Lys	Gly	Thr 355	Ile	Asp	Ile	Thr	Cys 360	Pro	Pro	Trp	Met	Asp 365	Trp	Phe	Phe
1319 1320 1321	Gly	Gly 370	Leu	Gln	Phe	Gln	Leu 375	Glu	His	His	Leu	Phe 380	Pro	Arg	Leu	Pro
1322 1323 1324	Arg 385	Gly	Gln	Leu	Arg	Lys 390	Ile	Ala	Pro	Leu	Ala 395	Arg	Asp	Leu	Cys	Lys 400
1325 1326 1327	Lys	His	Gly	Met	Pro 405	Tyr	Arg	Ser	Phe	Gly 410	Phe	Trp	Asp	Asp	Ala 415	Asn
1328 1329 1330	Val	Arg	Thr	Ile 420	Arg	Thr	Leu	Arg	Asp 425	Ala	Ala	Val	Gln	Ala 430	Arg	Asp
1331 1332 1333	Leu	Asn	Ser 435	Ala	Pro	Cys	Pro	Lys 440	Lys	Leu	Gly	Tyr	Gly 445	Glu	Ala	Туг
1334 1335 1336	Asn	Thr 450	His	Gly												

SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/08/934,254

DATE: 03/25/98 TIME: 16:50:25

Line	Егтог	Original Text
11 50	Number of Sequences (27) Doesn't Equal Actual Count (26) Entered (3588) and Calc. Seq. Length (0) differ	(iii) NUMBER OF SEQUENCES: 27 (A) LENGTH: 3588 base pairs
392	Entered (1884) and Calc. Seq. Length (0) differ	(A) LENGTH: 1884 base pairs
502	Entered (1685) and Calc. Seq. Length (0) differ	(A) LENGTH: 1685 base pairs
1053	Wrong Amino Acid Designator	2) INFORMATION FOR SEQ ID NO:26:
1053	Wrong Amino Acid Designator	2) INFORMATION FOR SEQ ID NO:26:
1053	Wrong Amino Acid Designator	2) INFORMATION FOR SEQ ID NO:26:
1053	Wrong Amino Acid Designator	2) INFORMATION FOR SEQ ID NO:26:
1053	Wrong Amino Acid Designator	2) INFORMATION FOR SEQ ID NO:26:
1056	Entered (1702) and Calc. Seq. Length (0) differ	(A) LENGTH: 1702 base pairs
1071	Wrong Sequence Number	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:
1239	Sequence 26 missing	(2) INFORMATION FOR SEQ ID NO:27:
1334	Stop Codon at end of sequence removed - no error	